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Dilmini Alahakoon

Anne Fennell

Jixiang Wu

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EVALUATING ADAPTIONS OF SOFT RED WINTER WHEAT IN EASTERN REGION OF USA

Dilmini Alahakoon, Anne Fennell, and Jixiang Wu
Department of Agronomy, Horticulture, and Plant Science
South Dakota State University, Brookings, SD 57007.

Abstract

Identification of winter wheat genotypes that are highly adapted to a wide range of environmental conditions is one of the most important wheat research objectives. Multi-environment trials (METs) under diverse environments is a commonly used practice to evaluate mean performance and yield stability. However, locations used and genotypes planted may vary from year to year which may cause yield stability analysis to be statistically challenging. In this study, we evaluated yield trial data containing 117 eastern soft red winter wheat genotypes that were grown in 35 locations in eastern production areas and four growing seasons (2012/2013 to 2015/2016). We used linear mixed model (LMM) and additive main effect and multiplicative interaction (AMMI) approaches to evaluate the mean performance and yield stability for each season. Genotype and location effects were highly significant at $\alpha = 0.001$ for all four seasons and location effects had higher variation compared to genotypic effects. For example, the proportional variance components for location and genotype effects varied from 58-78% and 4-11% among seasons. The first two PC score contribution ranged from 40.7 to 67.3 % to the total genotype-environment variation for all seasons. Both LMM and AMMI approaches detected that Branson, and MO080108-4 were better performers, thus these two methods were consistent.

Key words: stability analysis, eastern soft red winter wheat, linear mixed model, and additive main effect and multiplicative interaction

1. Introduction

Wheat is the principal food grain produced in the United States. Winter wheat production represents 70-80 % of total USA production (ERS, 2017). Among wheat crops, soft red winter wheat, accounting for 15-20 % of total production in USA, is grown primarily in states along the Mississippi River and in the eastern states. Flour from eastern soft red winter wheat (ESRWW) is mainly used for cakes, cookies, and crackers in the USA. To ensure consistent and nutritious food supply to the nation, continuous breeding programs aimed at developing varieties with improved grain yield, disease resistance, and end use quality are essential in these areas. Identification of high-yielding winter wheat cultivars that are widely adapted to diverse environmental conditions is highly desired.

Multi-environments trials (METs) under diverse environments are a commonly used practice to evaluate wheat yield stability. For example, uniform eastern and southern red soft winter wheat nursery trials are conducted annually by United States Department of Agriculture. Under this program, more than 30 ESRWW lines are evaluated annually for yield performance as well as many traits to predict their performance. Preferred genotypes for future use are expected to have high-yielding and stable performance in diverse locations and/or years (Gauch et al., 2008).

To identify the best genotype for a given location, genotype location interaction (GEI) can be used as a factor since it is the main component that affecting to the stability of a variety.

Because of the complex behaviour of GEI, a number of statistical methods have been proposed in order to quantify genotypic stability. Several commonly used statistical methods for yield stability analysis include Finlay and Wilkinson's (FW) regression coefficients (Finlay and Wilkinson, 1963), linear mixed model (LMM) approaches, genotype main effect and genotype environment interaction (GGE) biplot (Yan and Kang, 2003), and additive main effects and multiplicative interaction (AMMI) method (Gauch,1992).

The FW regression method allows us to compare the performance of set of varieties grown in different environments by linear regression coefficient and coefficient of determination. Because environment index (EI), which is used for yield stability evaluation is defined as the mean yield of all varieties for each environment and years. Yield stability is highly dependent on the varieties used in the trial. The AMMI method evaluates stability of crops by integrating both analysis of variance (ANOVA) and principal component analysis (PCA) to analyse METs. In this model, ANOVA is used to analyse genotype and environment main effects while PCA is for interactions between genotypes and environments (Silveria et al., 2012). GGE biplot analysis, which is based on PCA, is another effective method to explore the yield trials in different locations. It also allows visual examination of the relationships among the test environments, genotypes and the genotype environment interactions. Alternatively, statisticians have also applied ANOVA and LMM approaches to evaluate yield stability (Smith, 2005). The LMM approaches provide more flexibility to deal with complex models and missing and/or unbalanced data (Nuvunga et al., 2015).

The objective of this study was to evaluate yield stability for each ESRWW genotype in the recent four seasons of yield trials by using LMM approach and AMMI method and to determine those wheat genotypes that had both high-yielding potential and wide adaption in eastern area of USA. The yield trial data used in this study included 117 ESRWW, four growing seasons (2012/2013 to 2015/2016), and 35 locations across the eastern region of USA. The results will help to identify desirable winter wheat genotypes that are suitable in eastern region of USA.

2. Materials and Methods

2.1 Materials

The data set with 117 ESRWW genotypes that were grown in 35 locations, across 19 states in eastern region of USA, for four seasons (2012/13–2015/16) was used for this study. The data used in this study were individual genotypic means for each environment and were from Uniform Eastern Soft Red Winter Wheat Nursery Report published by United States Department of Agriculture.

2.2 Statistical analysis

First, we obtained genotypic and location means for grain yield and heading date across locations, genotypes, and seasons. Due to the large number of genotypes, we present mean trait values for only the top 25 genotypes in Table 2.

Due to highly unbalanced data structure across four growing seasons, we conducted separate LMM and AMMI analyses for each growing season. In addition, since only individual

genotypic means for each location were available, genotype-location interactions could not be separated from the model for each growing season. The linear model is as follows:

$$Y_{ij} = \mu + G_i + E_j + \varepsilon_{ij} \quad (1)$$

where Y_{ij} is the mean yield of genotype i in location j , μ is the population mean, G_i and E_j are the genotype and location effects and ε_{ij} is a residual including GEI that confounded with random error. In this study, we treated both genotype and location effects random.

Using LMM approaches, we calculated variance component, proportional variance component, estimated fixed effect, and predicted random effects for genotypes and locations. The standard error for each parameter was calculated with 10-fold jackknife resampling technique (Wu et al., 2012).

Though genotype-environment interaction in the model (1) could not be separated from the residual ε_{ij} , with the following AMMI model, it is possible to partially separate GEI effects (Zobel et al., 1988).

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^M \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij} \quad (2)$$

Y_{ij} , μ , G_i and E_j were defined in equation 1; λ_k is a singular value of the k axis in the PCA; α_{ik} and γ_{jk} are PC scores related to genotype and environmental factors, respectively; M is the number of principal components retained in the model; ρ_{ij} is the residual (Silveria et al, 2012).

We used R (version 3.3.2) statistical software under the RStudio (RStudio, 2016) environment to conduct LMM analysis (model 1) with the minque package (Wu, 2014) and AMMI analysis (model 2) with the agricolae package (Mendiburu, 2016).

3. Results and Discussion

3.1 Mean grain yield and heading date

According to Table 1, 39, 39, 31, and 30 genotypes and 21, 21, 24, and 24 locations were used in each season for the study. Genotypic mean across location for each season ranged from 72.47 to 79.51 bu/ac.

The top 25 genotypes recoded for highest mean yield and their heading date across all environments and years are shown in Table 2. The mean grain yield ranged from 96.44 to 81.2 bu/ac and their heading date ranged from 123.1 to 138.1 Julian days (Table 2). Hilliard, a check cultivar reported as the highest yielding genotype among all tested genotypes and Branson and MO080104, the other two check cultivars, showed comparatively higher mean yield of 81.85 and 82.47 bu/ac (Table 2). Hilliard was also reported as a high yielding variety in many states for state yield trials including Tennessee (West et al, 2016) and Wisconsin (Conley, 2016). As stated by Friesen et al (2015), forty-one (41) genotypes show mean grain yield greater than the population mean of 78.07 bu/ac (data not shown).

The top two locations with greater mean yield were Ithaca, NY (93.37 bu/ac) and Arlington, (WI) (92.63 bu/ac) (Table 3). Mead was reported with the lowest mean yield of 45.89 bu/ac among all locations. The season mean yield of genotypes across locations ranged from 72.47 to 79.51 bu/ac (Table 1), showing comparatively constant values across seasons. Since the breeders

selected the high yielding genotypes from new lines reported from these trials in each year, these results agreed with the study reported by Friesen et al (2015).

3.2 Variance components and genotypic effects

Significant location variance (58 – 78%) for four years was detected (Table 4), indicating that environmental conditions across different locations played a major role on grain yield. Campbell et al. (1976) reported the similar results in their study for Uniform ESRWW Nursery data. Genotypic effect contributed 4-11% of the total variance for different seasons. The results agreed with other published results (Dia et al, 2016 and Mohammadi et al, 2015). In 2015, Friesen et al also reported less than 10% genotypic variance for spring wheat (Friesen et al, 2015).

The checks Branson, MO080104, and Hilliard showed highest predicted effects for 2012/13, 2013/14, and 2015/16 seasons. The genotypic effects for Branson (2012/13), MO080104 (2013/14), and Hilliard (2015/16) were 5.7, 7.5 and 16 bu/ac, respectively (Table 5). Hilliard, Branson, and MO080104 found among genotypes with mean yield higher than 81.2 bu/ac in Table 2. The lowest effect for yield was -14.5 (reported in OH10-219-65 for 2015/16). The highest location effects for all seasons were 24 (Warsaw in 2012/13), 39 (Battle Ground in 2013/14), 30 (Urbana in 2014/15), and 29 (Arlington in 2015/16). The lowest (bottom 5) location effects were for Missouri, Illinois, Arkansas, Nebraska and Tennessee states more than one time (Table 5). Agreeing with Table 5, Table 3 showed Warsaw, Battle Ground, Urbana, and Arlington as high yielding locations and the reported mean yields are 80.46, 85.62, 90.42, and 92.63 bu/ac. Mead, (NE) (45.89 bu/ac), Marianna, (AK) (50.14 bu/ac), and Columbia, (MO) (53.76bu/ac) reported low mean yields among locations.

3.3 Stability analysis

AMMI biplot is constructed by plotting the first principal component (PC1) scores of the genotypes and the environments against their respective scores for the second principal component (PC2). Total contribution from PC1 and PC2 scores ranged from 45.8 to 67.3 % to the total GEI variance among four seasons (Figure 1a-d). Branson, MO080104 and Hilliard showed high yield for all seasons (Figure 2a-d). OH08-180-48, MO080104, MDC07026-F2-19-13-1, and Hilliard showed the highest mean yield for each season. Warsaw, Ithaca, Urbana, and Arlington were identified as high yielding locations in the present study by AMMI analysis. Low yielding locations for the four seasons were Milan, Marianna, Knoxville, and Columbia (Figure 1).

Highly stable genotypes located close to 0 in PC1 axis and for season 2012/13 highly stable genotypes were MD04W249-11-12, VA08MAS-369 (Figure 2a). Genotypes 0762A1-2-8 and OH07-263-3 were reported for highest stability in season 2013/14 (Figure 2b). Genotype TN 1505 located close to 0% (PC1) showing the highest stability for season 2014/15 (Figure 2c). Genotype 04620A1-1-7-4-17 showed highest stability for season 2015/16. Genotypes with high mean yield for season 2012/13 are LCS19228, Shirley and KWS008 and for season 2013/14 are LCS229, MO080104. MDC07026-F2-19-13-1 and MO121058 showed high mean performance for season 2014/15. In 2015/16 season, Hilliard, Branson, DH11SRW8-59 and OH09-207-68 report high mean performance. Moreover, these high performance varieties can be seen among top 25 genotypes (Table 2) and genotypes with high predicted effect (Table 5).

Two statistical approaches that we used to evaluate ESRWW genotypes are equally applicable for the present data. As for an example, in season 2012/13, 2013/14, and 2014/15, LMM

approach showed 5.22, 7.49, and 6.44 bu/ac predicted effects for MO080104 keeping among top five (Table 5). AMMI also graphed MO080104 in 2012/13, 2013/14, and 2014/15 seasons among high yielding genotypes (Figure 2a). Both these two methods have shown comparatively consistent results for most genotypes. Since LMM and AMMI derived from same parameters, this observation is acceptable (Piepho, 1998). For evaluation of ESRWW genotypes, we can use one of these two methods in future.

4. Conclusions

In this study, we applied both LMM and AMMI methods to analyse soft red winter wheat yield trial data including 117 genotypes, four growing seasons (2012/2013 to 2015/2016), and 35 locations across the eastern region of USA. Results showed that genotype and location effects were significant at $\alpha = 0.001$ for all tested seasons. Location effects showed a higher variation than genotypic effects (58-78% vs 4-11%). Check varieties performed well, showing the highest effects for three tested seasons. Contribution from the first two PC scores ranged from 40.7% to 67.3 % to the total GEI variation among seasons. Warsaw, Ithaca, Urbana and Arlington were high yielding locations while Knoxville, Columbia, Marianna and Milan were the lowest yielding locations. Branson, OH08-180-48, Hilliard, and DH11SRW8-59 showed higher yield than the population mean. The results were consistent between both LMM and AMMI approaches in the present study.

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Table 1. Number of genotypes, locations and mean yield for each season.

Season	Number of genotypes	Number of locations	Mean yield (bu/ac)
2012/13	39	21	72.48
2013/14	39	21	78.86
2014/15	31	24	72.47
2015/16	30	24	79.51

Table 2. Mean yield of top 25 genotypes across seasons and their heading date.

Genotype	Yield (bu/ac)	Heading date (Julian days)
Hilliard	96.44	125.23
DH11SRW8-59	94.12	127.98
MD09W272-8-4-14-6	88.36	124.60
KWS 078	87.57	127.04
OH09-207-68	87.32	124.74
VA11W-108	86.91	136.39
MD09W272-8-4-14-8	86.79	124.18
VA11W-313	86.58	121.67
KWS023	85.05	136.85
VA11W-279	84.76	123.10
MD09W272-8-4-13-3-15	84.66	123.54
MO110799	84.35	138.07
P0762A1-2-8	84.07	136.69
KWS024	83.84	137.74
LCS321	83.69	136.54
04620A1-1-7-4-17	83.39	127.45
LCS229	82.75	135.22
IL09-3264	82.59	134.62
P0722A1-1-7-4-17	82.49	136.73
MO080104	82.47	131.06
Branson	81.85	130.83
VA11W-230	81.66	135.75
MDC07026-F2-19-13-1	81.28	131.83
AR06050-7-2	81.26	125.09
IL07-18533-3	81.20	134.59

Table 3. Mean yield and heading date for each location across seasons.

Location	Yield (bu/ac)	Heading date (Julian days)
Ithaca	93.37	150.56
Arlington	92.63	NA
Logan Co	91.03	124.23
Urbana	90.42	136.92
West Lafayette	89.32	138.28
Griffin	87.93	109.29
Battle Ground	85.62	134.21
Raleigh	85.22	111.13
Champaign	84.31	139.16
Blacksburg	80.71	129.26
Warsaw	80.46	122.28
Napoleon	79.33	142.57
Clarksville	76.08	132.39
New Haven	75.96	142.45
Lafayette	74.57	139.75
Lexington	74.01	128.84
Oconto	73.36	NA
Knoxville	72.91	118.79
Ingham Co	72.52	NA
Nairn	71.89	155.14
Brownstown	71.28	NA
Harrisburg	69.24	130.69
Stuttgart	69.01	117.62
Mason	68.88	148.80
Schochoh	68.78	113.10
Winfield	67.43	NA
Webberville	64.34	153.71
Plymouth	63.43	115.79
Custar	63.02	142.97
Milan	58.20	NA
Columbia	53.76	133.66
Marianna	50.14	111.25
Mead	45.89	151.60
Clayton	NA	105.90
Windfall	NA	131.52

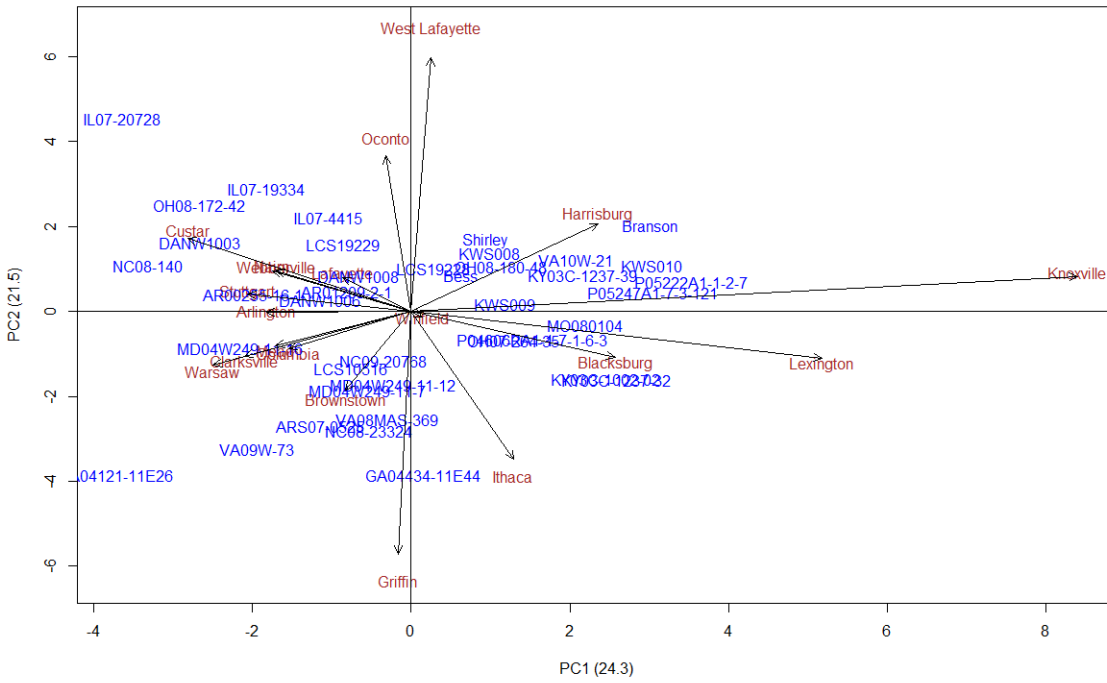
Table 4. Proportional variance components from LMM for location and genotype.

	Season			
	12/13	13/14	14/15	15/16
Location	0.58*	0.78*	0.77*	0.66*
Genotype	0.04*	0.04*	0.06*	0.11*
Error	0.38*	0.18*	0.17*	0.22*

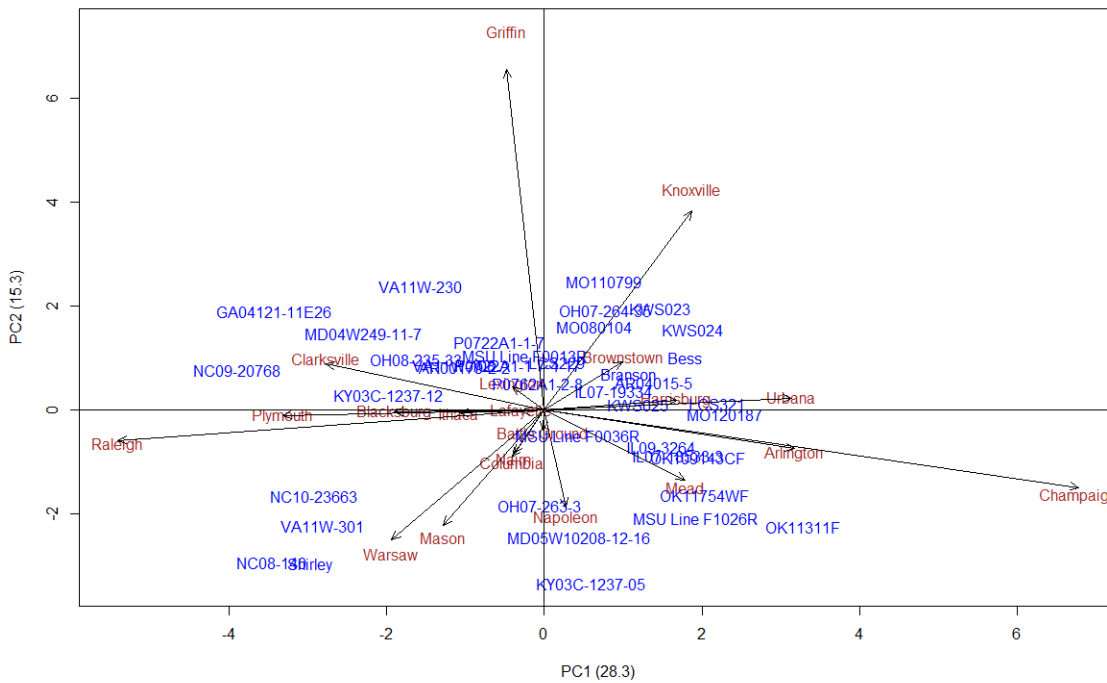
* Significant at 0.001

Table 5. The top 5 and bottom 5 (- sign) predicted random effects for genotypes and locations for all seasons.

Season	Genotype	Predicted effect	Location	Predicted effect
2012/13	Branson	5.69	Warsaw	23.92
	OH08-180-48	5.44	Ithaca	23.02
	Shirley	5.37	West Lafayette	20.51
	MO080104	5.22	Harrisburg	15.91
	VA10W-21	5.10	Griffin	15.90
	NC09-20768	-6.09	Knoxville	-20.15
	AR00255-16-1	-5.74	Columbia	-17.65
	GA04121-11E26	-5.51	Brownstown	-17.64
	ARS07-0525	-5.19	Winfield	-12.97
2013/14	MO080104	7.49	Battle Ground	38.92
	VA11W-108	7.26	Ithaca	28.75
	KWS023	5.58	Blacksburg	25.85
	IL07-19334	5.33	Griffin	22.91
	Branson	5.23	Clarksville	15.60
	OH07-264-35	-8.14	Mead	-41.18
	NC08-140	-7.47	Harrisburg	-29.04
	NC10-23663	-7.34	Champaign	-19.42
	MSU Line F0013R	-6.25	Columbia	-15.59
2014/15	MDC07026-F2-19-13-1	8.33	Urbana	29.93
	MO 121058	7.37	Champaign	23.40
	MO080104	6.44	Arlington	19.70
	VA11W-106	6.08	Logan Co.	18.49
	AR05094-4-1	4.53	Lafayette	16.89
	MD09W272-8-4-13-3	-11.99	Mead	-43.19
	OH07-206-69	-9.35	Columbia	-31.90
	IL02-19463-7	-6.54	Nairn	-24.92
	KY05C-1369-14-6-3	-6.45	Marianna	-20.31
2015/16	Hilliard	15.95	Arlington	29.05
	DH11SRW8-59	13.69	Urbana	28.54
	Branson	9.52	Nairn	27.03
	MD09W272-8-4-14-6	8.36	West Lafayette	26.74
	KWS 078	7.60	Champaign	24.96
	OH10-219-65	-14.50	Marianna	-31.18
	KY06C-1195-37-2-5	-13.83	Milan	-21.16
	TN1603	-12.97	Warsaw	-18.24
	Pioneer Brand 25R46	-12.51	Battle Ground	-17.12



a



b

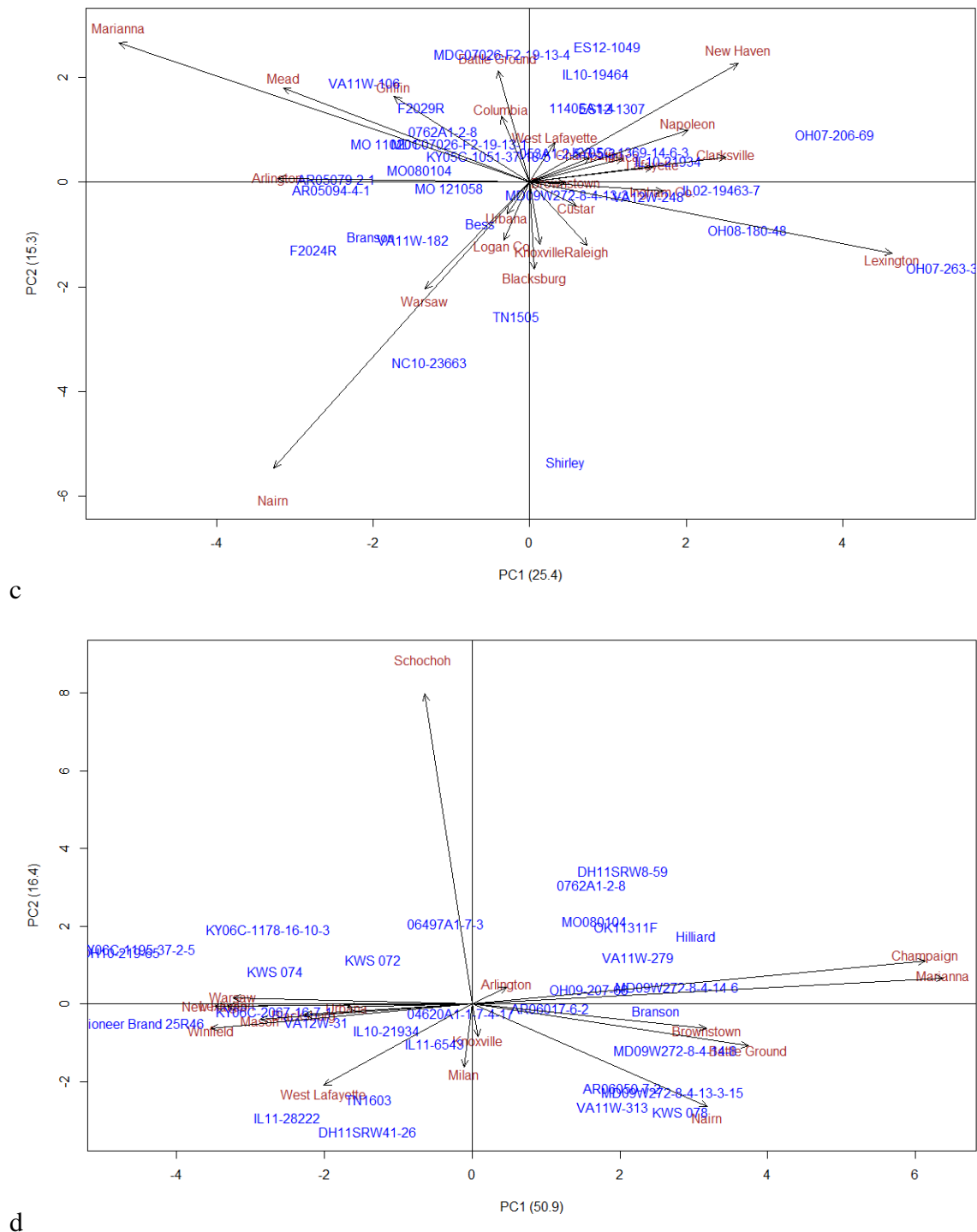
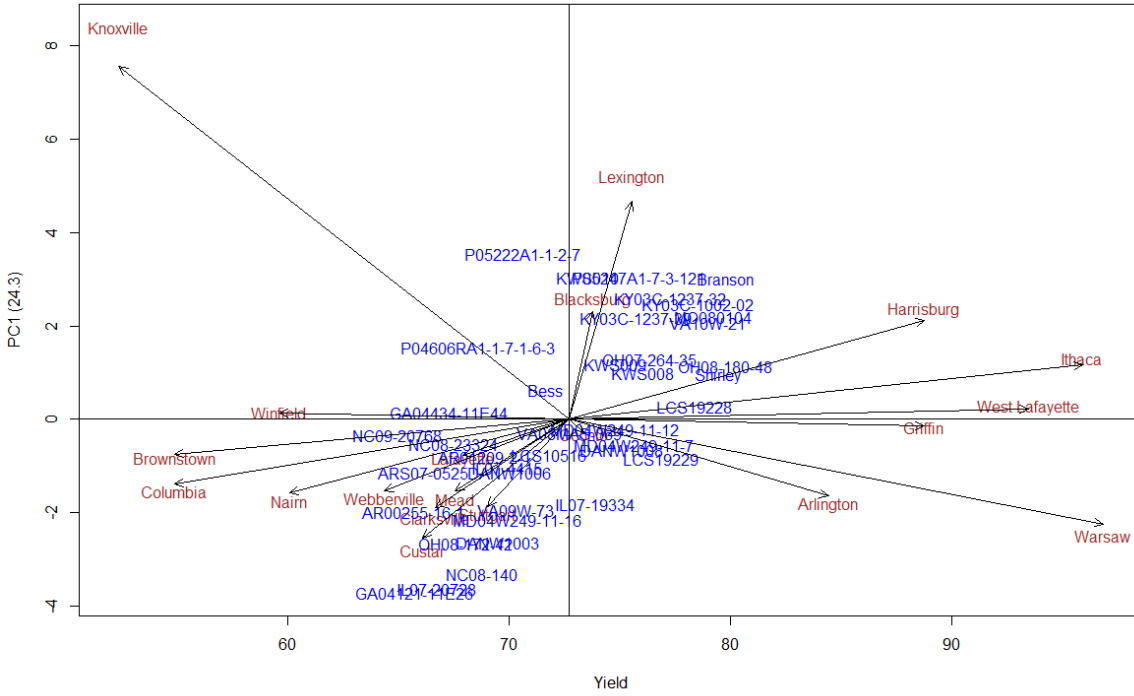
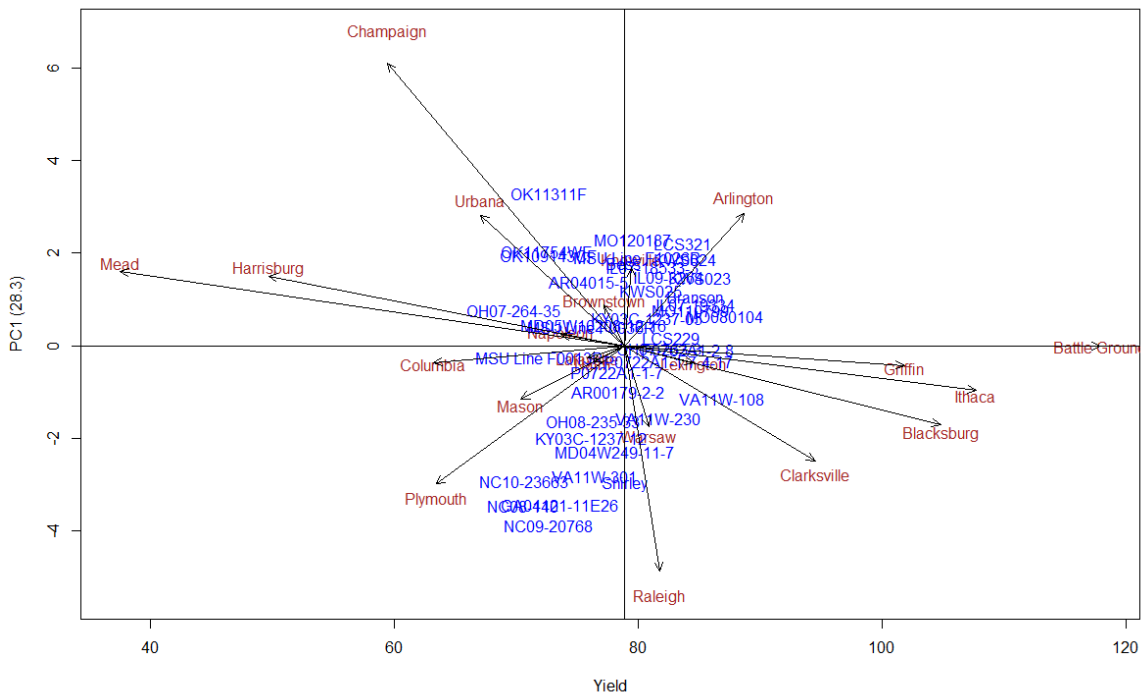


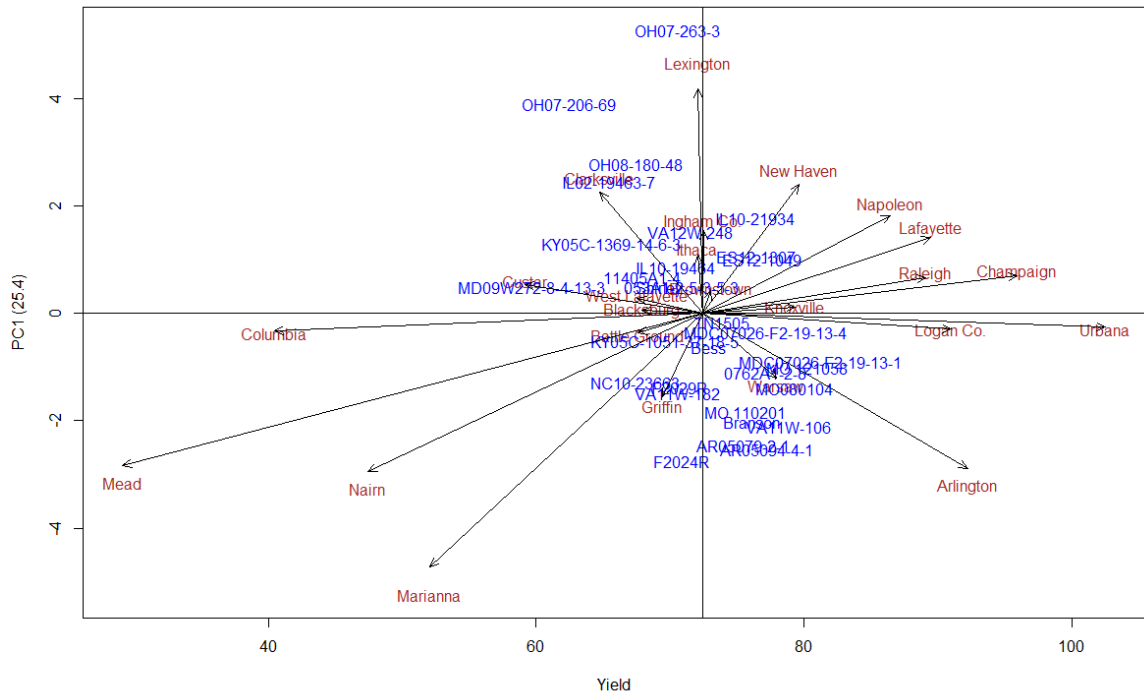
Figure 1. Principal component (PC1 and PC2) analysis plots for grain yield (bu/ac) of 39 genotypes and 21 locations for season 2012/13 (a), 2013/14 (b), 31 genotypes and 24 locations for season 2014/15 (c) and 30 genotypes and 24 locations for 2015/16 (d). Blue and red letters indicate genotypes and locations, respectively.



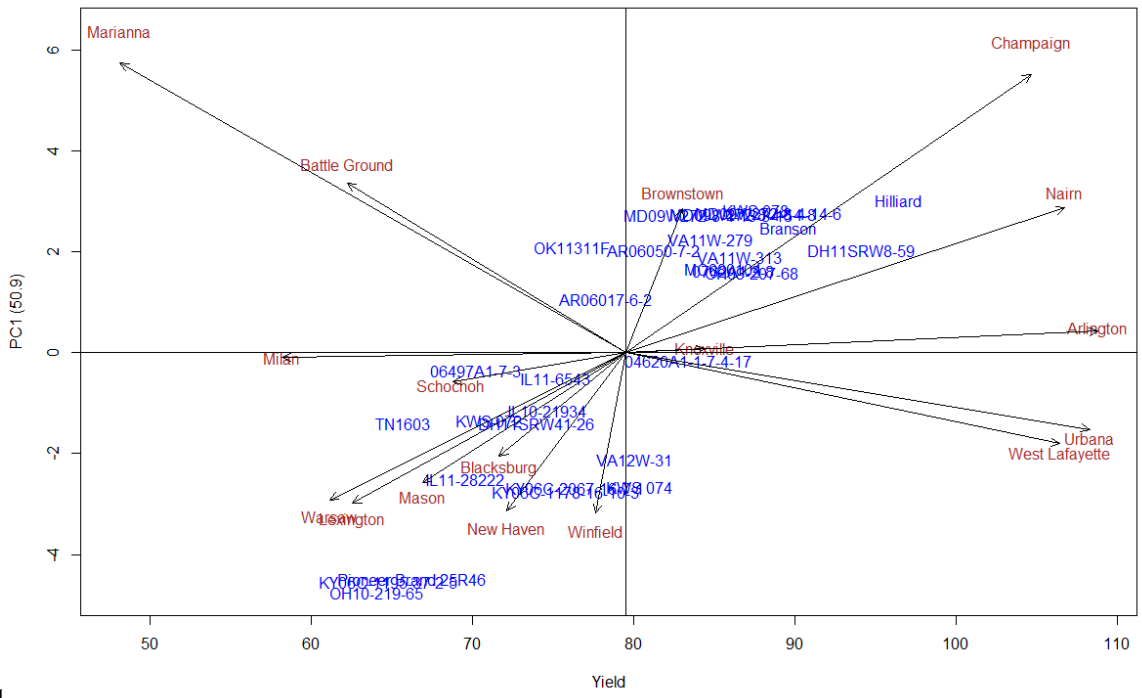
a



b



c



d

Figure 2. Genotype and GE interaction biplots for grain yield (bu/ac) of 39 genotypes and 21 locations for season 2012/13 (a), 2013/14 (b), 31 genotypes and 24 locations for season 2014/15 (c) and 30 genotypes and 24 locations for 2015/16 (d). Blue and red letters indicate genotypes and locations, respectively.